

| | | | | | | |
|--|-----|-----|-----|---------------|-----|-----|
| 5' NNG AAG GCT CAG CAT ACA CGT CGT GAC TTG GAA CGT GGC TTC GGC AGC GCC CCT | 9 | 18 | 27 | 36 | 45 | 54 |
| CGA GCT CTC AGT GAC CTG CTT CAG CTG AAC AAC CCG AAC CTC AAT CTT GAC ATA | 63 | 72 | 81 | 90 | 99 | 108 |
| TAT GTT ATT GGT TTG CAG GAA TTG AAC TCT GGG ATC ATA AGC CTC CTT TCC GAT | 117 | 126 | 135 | 144 | 153 | 162 |
| GCT GCC TTT AAT GAC TCG TGG AGC AGT TTC CTC ATG GAT GTG CTT TCC CCT CTG | 171 | 180 | 189 | 198 | 207 | 216 |
| | | | | M D V L S P L | | |
| AGC TTC ATC AAG GTC TCC CAT GTC CGT ATG CAG GGG ATC CTC TTA CTG GTC TTT | 225 | 234 | 243 | 252 | 261 | 270 |
| S F I K V S H V R M Q G I L L L V F | | | | | | |
| GCC AAG TAT CAG CAT TTG CCC TAT ATC CAG ATT CTG TCT ACT AAA TCC ACC CCC | 279 | 288 | 297 | 306 | 315 | 324 |
| A K Y Q H L P Y I Q I L S T K S T P | | | | | | |
| ACT GGC CTG TTT GGG TAC TGG GGG AAC AAA GGT GGA GTC AAC ATC TGC CTG AAG | 333 | 342 | 351 | 360 | 369 | 378 |
| T G L F G Y W G N K G G V N I C L K | | | | | | |

FIGURE 1A

| | | | | | | |
|-----|---|-----|-----|-----|-----|-----|
| 387 | CTT TAT GGC TAC TAT GTC | 396 | 405 | 414 | 423 | 432 |
| | L Y G Y Y V S I I N C H L P P H I S | | | | | |
| 441 | AAC AAT TAC CAG CGG CTG GAG CAC TTT | 450 | 459 | 468 | 477 | 486 |
| | N N Y Q R L E R I L E F D R I L E M Q N C | | | | | |
| 495 | GAG GGG CGA GAC ATC CCA AAC ATC CTG GAC CAC GAC CTC ATT ATC TGG TTT GGA | 504 | 513 | 522 | 531 | 540 |
| | E G R D I P N I L D H D L I I W F G | | | | | |
| 549 | GAC ATG AAC TTT CGG ATC GAG GAC TTT GGG TTG CAC TTT GTT CGG GAA TCC ATT | 558 | 567 | 576 | 585 | 594 |
| | D M N F R I E D F G L H F V R E S I | | | | | |
| 603 | AAA AAT CGG TGC TAC GGT GGC CTG TGG GAG AAG GAC CAG CTC AGC ATT GCC AAG | 612 | 621 | 630 | 639 | 648 |
| | K N R C Y G G L W E K D Q L S I A K | | | | | |
| 657 | AAA CAT GAC CCG CTG CTC CGG GAG TTC CAG GAG GGC CGC CTA CTC TTC CCG CCC | 666 | 675 | 684 | 693 | 702 |
| | K H D P L L R E F Q E G R L L F P P | | | | | |
| 711 | | 720 | 729 | 738 | 747 | 756 |

FIGURE 1B

| | |
|---|------|
| ACC TAC AAG TTT GAT AGG AAC TCC AAC GAC TAT GAC ACC AGT GAG AAA AAA CGC | |
| T Y K F D R N S N D Y D T S E K K R | |
| 765 | |
| AAG CCT GCA TGG ACC GAT CGC ATC CTG TGG AGG CTG AAG CGG CAG CCC TGT GCT | 801 |
| K P A W T D R I L W R L K R Q P C A | 810 |
| 819 | |
| GGC CCC GAC ACT CCC ATA CCG CCG GCG TCA CAC TTC TCC TTG TCT CTG AGG GGC | 855 |
| G P D T P I P P A S H F S L S L R G | 864 |
| 873 | |
| TAC AGC AGC CAC ATG ACG TAC GGC ATC AGC GAC CAC AAG CCT GTC TCC GGC ACG | 909 |
| Y S S H M T Y G I S D H K P V S G T | 918 |
| 927 | |
| TTC GAC TTG GAG CTG AAG CCA TTG GTG TCT GCT CCG CTG ATC GTC CTG ATG CCC | 963 |
| F D L E L K P L V S A P L I V L M P | 972 |
| 981 | |
| GAG GAC CTG TGG ACC GTG GAA AAT GAC ATG ATG GTC AGC TAC TCT TCA ACC TCG | 1017 |
| E D L W T V E N D M M V S Y S S T S | 1026 |
| 1035 | |
| 1044 | |
| 1053 | |
| 1062 | |
| 1071 | |
| 1080 | |

FIGURE 1C

| | | | | | |
|---|------|------|------|------|------|
| GAC TTC CCC AGC AGC CCG TGG GAC TGG ATT GGA CTG TAC AAG GTG GGG CTG CCG | | | | | |
| D F P S S P W D W I G L Y K V G L R | | | | | |
| 1089 | 1098 | 1107 | 1116 | 1125 | 1134 |
| GAC GTT AAT GAC TAC GTG TCC TAT GCC TGG GTC GGG GAC AGC AAG GTC TCC TCC | | | | | |
| D V N D Y V S Y A W V G D S K V S C | | | | | |
| 1143 | 1152 | 1161 | 1170 | 1179 | 1188 |
| AGC GAC AAC CTG AAC CAG GTT TAC ATC GAC ATC AGC AAT ATC CCT ACC ACT GAA | | | | | |
| S D N L N Q V Y I D I S N I P T E | | | | | |
| 1197 | 1206 | 1215 | 1224 | 1233 | 1242 |
| GAT GAG TTT CTC CTC TGT TAC TAC AGC AAC AGT CTG CGT TCT GTG GTG GGG ATA | | | | | |
| D E F L L C Y Y S N S L R S V V G I | | | | | |
| 1251 | 1260 | 1269 | 1278 | 1287 | 1296 |
| AGC AGA CCC TTC CAG ATC CCG CCT GGC TCC TTG AGG GAG CCA CTG GGT GAA | | | | | |
| S R P F Q I P P G L R E D P L G E | | | | | |
| 1305 | 1314 | 1323 | 1332 | 1341 | 1350 |
| GCA CAG CCA CAG ATC TGA GCC AGG ATG GGA GTG AAT CCC AGG CCG AGG CCA GAG | | | | | |
| A Q P Q I | | | | | |
| 1359 | 1368 | 1377 | 1386 | 1395 | 1404 |
| CTG GCA GCC AGC TCT GCC TTT CCA CTG CCG GGA GTG CTG GGG GCC CAG CCT GGC | | | | | |

FIGURE 1D

| | | | | | |
|---|------|------|------|------|------|
| 1413 | 1422 | 1431 | 1440 | 1449 | 1458 |
| CCC CTG AAG AGA CAG CCA AGT GTC GTC CAC ATA CTC CTC CCA GAG TGA GCT CTA | | | | | |
| 1467 | 1476 | 1485 | 1494 | 1503 | 1512 |
| ACC AGG CTC ATT TGC TCT CTC CAC TAC TCA TCT CTG GAA TTA GCC GCT TAA ATA | | | | | |
| 1521 | 1530 | 1539 | 1548 | 1557 | 1566 |
| CAG GTT TTT GTT GCT GAG ATG TGA GTG AAA CCA GCT AGT GTG TCA ACA GTG AAG | | | | | |
| 1575 | 1584 | 1593 | 1602 | 1611 | 1620 |
| ACC TGG GGA CAG TTC TGC GTC TCA TTT CTG GAT TCC TAC CCC CTC TTC TAG TCT | | | | | |
| 1629 | 1638 | 1647 | 1656 | 1665 | 1674 |
| TGC CCA AGT AGT CCT GCC AGG CAC ATG CCC CAT TTG GCA CAG GCC TGC ATT CTT | | | | | |
| 1683 | 1692 | 1701 | 1710 | 1719 | 1728 |
| GTC GTG CCG TCC TGG GCC TCA GGC TGT CTG GGA GGG GAG ATG CTC ACA TTT GTA | | | | | |
| 1737 | 1746 | 1755 | 1764 | 1773 | 1782 |
| CAG GCT ACA TAG ACT GGT GCA AGC AGT GCT GGA TTC CAG GAG TCT TGG CAT CTC | | | | | |
| 1791 | 1800 | 1809 | 1818 | 1827 | 1836 |
| ATA GCT TGT CCC CGT GAG GAG TGA GCA GAG GGT CTG GGA TTT CTG CTT TCA GCA | | | | | |

FIGURE 1E

| | | | | | |
|---|------|------|------|------|------|
| 1845 | 1854 | 1863 | 1872 | 1881 | 1890 |
| AAA GCA GTC TGA CTC AGT GGG CAG AAT GGA GGG GCC CCT CTA GCC AGG CTC TTA | | | | | |
| 1899 | 1908 | 1917 | 1926 | 1935 | 1944 |
| CGC CAT GGT TAT GAG CAG GTT GAT GAG GGT CCT TCG GCC AGC ACA ACC TTC CTC | | | | | |
| 1953 | 1962 | 1971 | 1980 | 1989 | 1998 |
| CCT ACT CAC GGC ATG GAG TCT GAC TGC ATG GAA GTT CCA GAT CCT GAC AGA GAG | | | | | |
| 2007 | 2016 | 2025 | 2034 | 2043 | 2052 |
| AAC TGG GAA GGA TCC AGG TTC GCT TCC GTT GGT AGC TTG AGT CCC ATG CCT CCA | | | | | |
| 2061 | 2070 | 2079 | 2088 | 2097 | 2106 |
| CCC TGC CAT CTG AGG AAG GGG TGA CAA GTG GTC AAG GAG CTG TGG CCA CAG ACT | | | | | |
| 2115 | 2124 | 2133 | 2142 | 2151 | 2160 |
| TTT CCA GGG TGG TCC TTG GCA GGT GAG GTG CGT CTG TGC CAC CCT TGT CAG GAG | | | | | |
| 2169 | 2178 | 2187 | 2196 | 2205 | 2214 |
| TCA TTG ACG ACG GGC CCC CCC TGG ACC CCC CGG GAC CTC AGA GTG GGG GCA GGC | | | | | |
| 2223 | 2232 | 2241 | 2250 | 2259 | 2268 |
| AGA AGG GAG AAC CAG CTC AAG ACA TTT TGG AGG ATC TGG CCC TGG GGT TCT TCA | | | | | |

FIGURE 1F

| | | | | | |
|---|------|------|------|------|------|
| 2277 | 2286 | 2295 | 2304 | 2313 | 2322 |
| GAG AAC ACC CTC TAG GGG CTT TGG GGA CAT GGC CTG TCC CCA CAT CCA GCA CTT | | | | | |
| 2331 | 2340 | 2349 | 2358 | 2367 | 2376 |
| GCC TCC GCC ATG GTC ACT CGG CAG CCC TTT TCC CAG GAG AAG ACA CCT CTG GGA | | | | | |
| 2385 | 2394 | 2403 | 2412 | 2421 | 2430 |
| GCC TGC TCA GTG CTT GTC CTG CCA TCC TGT GTC CTG GGA CTG AGG GTT ACT CCA | | | | | |
| 2439 | 2448 | 2457 | 2466 | 2475 | 2484 |
| GTT GCT CTG TGT TGC ATA CTC TCC CCC GCA AGC CTG TGT ATG AAG AAT TGT CCC | | | | | |
| 2493 | 2502 | 2511 | 2520 | 2529 | 2538 |
| CTG GCT TCC AGC AGG CCA TGG CTG GCT GTT TTG TGA CTG TTA CAT TGT GCA GGG | | | | | |
| 2547 | 2556 | 2565 | 2574 | | |
| GTA ATT ATT AGC GTG GCT TTT ACA CTT AAA AAA AAA A 3' | | | | | |

FIGURE 1G

[illegible]

FIGURE 2A

9 - - - - - 638789
 3 - - - - -
 236 L Q P R Q N K S K S E I T D M V - R S S T I T V S D K A H I L S - - - - - g1399105
 173 I H R E P P P P F S V N K M L P R E K E A S N K E Q P K V T N T M R K L F V P - - - - - g1019103
 g1420920
 9 - - - - - 638789
 3 - - - - -
 271 - - - - - G L R D T I V K S H L L Q K E E D Y T Y I Q N F R F F A G T Y N V N G Q - - - - - g1399105
 213 N T Q S G Q R E G L I K H I L A K R E K E Y V N I Q T F R F F V G T W N V N G Q - - - - - g1019103
 g1420920
 9 - - - - - 638789
 3 - - - - -
 307 S P K E C L R L W L S N G I Q A P D V Y C V G F Q E L D L S K E A F F F H D T P - - - - - g1399105
 253 S P D S G L E P W L N C D P N P P D I Y C I G F Q E L D L S T E A F F Y F E S V - - - - - g1019103
 g1420920
 9 - - - - - 638789
 3 - - - - -
 347 K E E E W F K A V S E G L H P D A K Y A K V K L I R L V G I M L L L Y V K Q E H - - - - - g1399105
 293 K E Q E W S M A V E R G L H S K A K Y K V Q L V R L V G M M L L I F A R K D Q - - - - - g1019103
 g1420920
 31 L P Y I O I L S T K S T P T G L F G Y W G N K G G V N I C L K L Y G Y Y V S I - - - - - 638789
 3 - - - - -
 387 A A Y I S E V E A E T V G T G I M G R M G N K G G V A I R F Q F H N T S I C V V - - - - - g1399105
 333 C R Y I R D I A T E T V G T G I M G K M G N K G G V A V R F V F H N T T F C I V - - - - - g1019103
 g1420920
 71 N C H L P P H I S N N Y O R L E H F D R I - L E M O N C E - G R D I P - - N I L - - - - - 638789
 3 - - - - -
 427 N S H L A A H I E E Y E R R N Q D Y K D I C S R M Q F Q Q P D P S L P L T I S - - - - - g1399105
 373 N S H L A A H V E D F E R R N Q D Y K D I C A R M S F V V P N Q T L P Q L N I M - - - - - g1019103
 g1420920

FIGURE 2B

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----------|-----------|---|-----------|---|---|---|---|---|
| 107 | D | H | D | L | I | I | W | F | G | D | M | N | F | R | I | E | D | F | G | L | H | F | V | R | E | S | I | K | N | R | C | Y | G | G | L | W | E | K | D | Q | 638789 | | | | | | | |
| 3 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | gi1399105 | | | | | | | | |
| 467 | N | H | D | V | I | L | W | L | G | D | L | N | Y | R | I | E | E | L | D | V | E | K | V | K | K | L | I | E | E | K | D | F | Q | M | L | Y | A | Y | D | Q | gi019103 | | | | | | | |
| 413 | K | H | E | V | I | W | L | G | D | L | N | Y | R | L | C | M | P | D | A | N | E | V | K | S | L | I | N | K | K | D | L | Q | R | L | L | K | F | D | Q | gi420920 | | | | | | | | |
| 147 | L | S | I | A | K | K | H | D | P | L | L | R | E | F | Q | E | G | R | L | L | F | P | P | T | Y | K | F | D | R | N | S | N | D | Y | D | T | S | E | K | K | 638789 | | | | | | | |
| 25 | L | N | M | A | K | N | T | W | F | I | L | K | G | F | Q | E | G | P | L | N | F | A | P | T | F | K | F | D | V | G | T | N | K | Y | D | T | S | A | K | K | gi1399105 | | | | | | | |
| 507 | L | K | I | Q | V | A | A | K | T | V | F | E | G | F | T | E | G | E | L | T | F | Q | P | T | Y | K | Y | D | T | G | S | D | W | D | T | S | E | K | C | gi019103 | | | | | | | | |
| 453 | L | N | I | Q | R | T | Q | K | K | A | F | V | D | F | N | E | G | E | I | K | F | I | P | T | Y | K | Y | D | S | K | T | D | R | W | D | S | S | G | K | C | gi420920 | | | | | | | |
| 187 | R | K | P | A | W | T | D | R | I | L | W | R | L | K | R | Q | P | C | A | G | P | D | T | P | I | P | P | A | S | H | F | S | L | S | L | R | G | Y | S | S | 638789 | | | | | | | |
| 65 | R | K | P | A | W | T | D | R | I | L | W | K | V | K | - | A | P | G | G | G | P | S | P | S | G | R | K | S | H | R | L | Q | V | T | Q | H | S | Y | R | S | gi1399105 | | | | | | | |
| 547 | R | A | P | A | W | C | D | R | I | L | W | K | G | K | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | gi019103 | | | | | | | |
| 493 | R | V | P | A | W | C | D | R | I | L | W | R | G | T | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | gi420920 | | | | | | | |
| 227 | H | M | T | Y | G | I | S | D | H | K | P | V | S | G | T | F | D | L | E | L | K | P | L | V | S | A | P | L | I | V | L | M | P | E | D | L | W | T | V | - | 638789 | | | | | | | |
| 104 | H | M | E | Y | T | V | S | D | H | K | P | V | A | Q | F | L | L | Q | F | A | F | R | V | D | D | M | P | L | V | R | L | E | V | A | D | E | W | V | R | - | gi1399105 | | | | | | | |
| 570 | H | M | A | L | K | T | S | D | H | K | P | V | S | V | F | D | I | G | V | R | V | N | D | E | L | Y | R | K | T | L | E | I | V | R | S | L | D | g | i | 0 | 1 | 9 | 1 | 0 | 3 | | | |
| 516 | H | M | E | L | K | T | S | D | H | K | P | V | S | A | L | F | H | I | G | V | K | V | V | D | E | R | R | Y | R | K | V | F | E | D | S | V | R | I | M | D | g | i | 4 | 2 | 0 | 9 | 2 | 0 |
| 266 | - | - | E | N | D | M | M | V | S | Y | S | S | T | S | - | D | F | P | S | S | P | W | D | W | I | G | L | Y | K | V | G | L | R | D | V | N | D | - | - | - | - | - | 638789 | | | | | |
| 143 | - | - | P | E | Q | A | V | R | Y | R | M | E | T | - | V | F | A | R | S | S | W | D | W | I | G | L | Y | R | V | G | F | R | H | C | K | D | - | - | - | - | - | - | gi1399105 | | | | | |
| 610 | K | M | E | N | A | N | I | P | S | V | S | L | S | K | R | E | F | C | F | Q | N | V | K | Y | M | Q | L | K | V | E | S | F | T | I | - | H | N | G | Q | V | g | i | 0 | 1 | 9 | 1 | 0 | 3 |
| 556 | R | M | E | N | D | F | L | P | S | L | E | L | S | R | R | E | F | V | F | E | N | V | K | F | R | Q | L | Q | K | G | K | F | I | S | N | N | G | Q | V | g | i | 4 | 2 | 0 | 9 | 2 | 0 | |
| 300 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | 638789 | | | | | |
| 177 | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | gi1399105 | | | | | |
| 649 | P | C | H | F | E | F | I | N | K | P | D | E | E | S | Y | C | K | Q | W | L | N | A | N | P | S | R | G | F | L | P | D | S | D | V | E | I | D | L | E | g | i | 0 | 1 | 9 | 1 | 0 | 3 | |
| 596 | P | C | H | F | S | F | I | P | K | L | N | D | S | Q | Y | C | K | P | W | L | R | A | E | P | F | E | G | Y | L | E | P | N | E | T | V | D | I | S | L | D | g | i | 4 | 2 | 0 | 9 | 2 | 0 |

FIGURE 2C

| | | | | | | |
|-----|---|-----------|-----------|-----------|---------|----------|
| 317 | L N Q V Y I D I S N I P T T E D | - - - - - | - - - - - | - - - - - | - [E F] | 638789 |
| 192 | T Y Q V T F S E E S L P K G H G | - - - - - | - - - - - | - - - - - | - [D F] | g1399105 |
| 689 | [L] F V N K T T A T K L N S G E D K I E D I L V L H L D R G K D Y F L S V S G N Y | - - - - - | - - - - - | - - - - - | - | g1019103 |
| 636 | V Y V S K D S V T I L N S G E D K I E D I L V L H L D R G K D Y F L T I S G N Y | - - - - - | - - - - - | - - - - - | - | g1420920 |
| 335 | [L] L C Y Y S N S L R S V V G I S R P F | - - - - - | - - - - - | - - - - - | - | 638789 |
| 210 | I [J] G Y Y S H N H S I L I G I T E P F | - - - - - | - - - - - | - - - - - | - | g1399105 |
| 729 | L P S C F G S P I H T L C Y M R E P I L D L P | - - - - - | - - - - - | - - - - - | - | g1019103 |
| 676 | [L] P S C F G T [S] E A L C R M K R P I R E V P | - - - - - | - - - - - | - - - - - | - | g1420920 |
| 357 | - - - - - | - - - - - | - - - - - | - - - - - | - | 638789 |
| 248 | S - - - - S E G E D D S T L E - - - L L A P K S R S P S P G K S K R H R S R S P G | - - - - - | - - - - - | - - - - - | - | g1399105 |
| 759 | T L M P V W T G D D G S Q L D S P M E I P K E L W M V D Y L Y R N A V Q Q E D | - - - - - | - - - - - | - - - - - | - | g1019103 |
| 716 | S L L Q M V P L D E G A S - E R P L Q V P K E I W L V D H L F K Y A C H Q E D | - - - - - | - - - - - | - - - - - | - | g1420920 |
| 357 | - - - - - | - - - - - | - - - - - | - - - - - | - | 638789 |
| 282 | L A R F P G L A - - - - - | - - - - - | - - - - - | - - - - - | - | g1399105 |
| 799 | L F Q Q P G L R S E F E H I R D C L D T G M I D N L S A S N H S V A E A L L F | - - - - - | - - - - - | - - - - - | - | g1019103 |
| 755 | L F Q T P G M Q E E L Q I I D C L D T S I P E T I P G S N H S V A E A L L I F | - - - - - | - - - - - | - - - - - | - | g1420920 |
| 357 | - - - - - | - - - - - | - - - - - | - - - - - | - | 638789 |
| 313 | R V A - P D R S S N G S S R G S S E E G P S G L P G P W A F P A V P R S - - - | - - - - - | - - - - - | - - - - - | - | g1399105 |
| 839 | L E S L P E P V I C Y S T Y H N C L E C S G N Y T A S K Q V I S T L P I F H K N | - - - - - | - - - - - | - - - - - | - | g1019103 |
| 795 | L E A L P E P V I C Y E L Y Q R C L D S A Y D P R I C R Q V I S Q L P R C H R N | - - - - - | - - - - - | - - - - - | - | g1420920 |
| 357 | - - - - - | - - - - - | - - - - - | - - - - - | - | 638789 |
| 349 | - - - - - L G L L P A L - R L E T V D P G G G S W G P D R E A L - - - - | - - - - - | - - - - - | - - - - - | - [P G] | g1399105 |
| 879 | V F H Y L M A F L R E L L K N S A K N H L D E N I L A S I F G S L L L R N P A [G] | - - - - - | - - - - - | - - - - - | - | g1019103 |
| 935 | V F R Y L M A F L R E L L K F S E Y N S V N A M I A T L F T S L L L R P P [N] | - - - - - | - - - - - | - - - - - | - | g1420920 |

FIGURE 2D

T09290* 28226860

359 SLREDP-----LGEAQPQI
379 SLSPSPQGHR-----GLEGGGLGP
919 H-QKLDMTKKKAQEFIHQFL--CNPL
875 LMARQTPSDRQRAIQFLGLGSEED

638789
g1399105
g1019103
g1420920

FIGURE 2E

| Library | Lib Description | Abun | Pct Abun |
|------------|--|------|----------|
| PANCLSM01 | pancreas, islet cells, NORM, WM | 2 | 0.1907 |
| SCORNON01 | spinal cord, 71 M, NORM | 1 | 0.1379 |
| BSTWNOT01 | brain stem, 72 M | 1 | 0.1214 |
| MUSCNOT01 | skeletal muscle, WM | 2 | 0.0861 |
| THPINOT01 | THP-1 promonocyte cell line, untreated | 1 | 0.0571 |
| SYNORAT01 | synovium, elbow, rheumatoid, 51 F | 1 | 0.0478 |
| NERVMSM01 | multiple sclerosis, 46 M, NORM, WM | 2 | 0.0448 |
| BRSTWOT03 | breast, 54 F, match to BRSTTUT02 | 3 | 0.0441 |
| PENCNOT01 | penis, corpus cavernosum, 53 M | 1 | 0.0394 |
| COLANNOT09 | colon, 60 M, match to COLNTUT16 | 1 | 0.0390 |
| PROSNOT20 | prostate, 65 M, match to PROSTUT12 | 1 | 0.0336 |
| COLNNOT13 | colon, ascending, 28 M | 1 | 0.0311 |
| BRAITUT08 | brain tumor, astrocytoma, 47 M | 2 | 0.0293 |
| SCORNOT04 | spinal cord, 32 M | 1 | 0.0293 |
| LEUKNOT02 | white blood cells, 45 F | 1 | 0.0292 |
| COLNFET02 | colon, fetal F | 2 | 0.0286 |
| THVRTUT03 | thyroid tumor, benign, 17 M | 1 | 0.0276 |
| LNODNOT05 | lymph nodes, 14 F | 1 | 0.0271 |
| THP1AZS08 | THP-1 promonocyte cell line, treated AZ, SUB | 2 | 0.0269 |
| UTRSNOT08 | uterus, endometrium, 35 F | 1 | 0.0267 |
| HEAANOT01 | heart, coronary artery, 46 M | 1 | 0.0265 |
| HEAONOT03 | heart, aorta, 27 F | 1 | 0.0265 |
| BRAITUT13 | brain tumor, meningioma, 68 M | 1 | 0.0262 |
| COTRNOT01 | colon, transverse, Crohn's, 26 M | 1 | 0.0260 |

FIGURE 3A

| | | | |
|------------|--|---|--------|
| BONRFET01 | rib, fetal M | 1 | 0.0259 |
| SINTFET03 | small intestine, fetal F | 2 | 0.0259 |
| THYMNON04 | thymus, 3 M, NORM | 1 | 0.0257 |
| STOMFET01 | stomach, fetal F | 1 | 0.0255 |
| TYLMN0T02 | lymphocytes (non-adher PBMC), M/F | 1 | 0.0254 |
| HEAON0T05 | heart, aorta, 17 F | 1 | 0.0252 |
| UTRSTUT04 | uterine tumor, leiomyoma, 34 F | 1 | 0.0250 |
| LUNGUT013 | lung tumor, adenocarcinoma, 47 M | 1 | 0.0249 |
| PONSAT01 | brain, pons, Alzheimer's, 74 M | 1 | 0.0249 |
| TMLR3DT02 | lymphocytes (non-adher PBMC), M/F, 72-hr MLR | 1 | 0.0246 |
| PROSN0T15 | prostate, 66 M, match to PROSTUT10 | 1 | 0.0241 |
| SINJN0T02 | small intestine, jejunum, 8 F | 1 | 0.0241 |
| UCMCN0T02 | mononuclear cells | 1 | 0.0236 |
| LIVSFEM03 | liver/spleen, fetal M, NORM, WM | 1 | 0.0214 |
| BRSTNOM02 | breast, F, NORM, WM | 1 | 0.0206 |
| BRSTTUT03 | breast tumor, 58 F, match to BRSTN0T05 | 2 | 0.0197 |
| COLNLTUT03 | colon tumor, 62 M, match to COLNNT016 | 1 | 0.0196 |
| THYMN0T02 | thymus, 3 M | 1 | 0.0194 |
| HNT3AZT01 | hNT2 cell line, teratocarcinoma, treated AZ | 1 | 0.0191 |
| NEUTLPT01 | granulocytes, periph blood, M/F, treated LPS | 1 | 0.0173 |
| MUSCN0T07 | muscle, forearm, 38 F | 1 | 0.0154 |
| COLNNT011 | colon, 60 M, match to COLNLTUT16 | 1 | 0.0149 |
| NGANN0T01 | ganglioneuroma, 9 M | 2 | 0.0146 |
| PROSTUT05 | prostate tumor, 69 M, match to PROSN0T07 | 1 | 0.0145 |
| THYR0T03 | thyroid tumor, adenoma, 28 F | 1 | 0.0138 |
| SPLNNT0T4 | spleen, 2 M | 1 | 0.0128 |

FIGURE 3B

| | | | |
|-----------|---|---|--------|
| KIDNNOT05 | kidney, neonatal F | 1 | 0.0106 |
| EOSIHT02 | eosinophils, hypereosinophilia, 48 M | 1 | 0.0105 |
| OVARTUT01 | ovarian tumor, 43 F, match to OVARNOT03 | 1 | 0.0103 |
| UTRPNOM01 | uterus, F, NORM, WM | 1 | 0.0101 |
| MELANOM01 | melanocytes, M, NORM, WM | 1 | 0.0096 |
| BRSTTUT01 | breast tumor, 55 F, match to BRSTNOT02 | 1 | 0.0095 |
| BRAINOM01 | brain, infant F, NORM, WM | 2 | 0.0089 |
| CARDFEM01 | heart, fetal, NORM, WM | 1 | 0.0082 |
| UTRSNOT02 | uterus, 34 F | 1 | 0.0078 |
| LUNGFET03 | lung, fetal F | 1 | 0.0069 |
| PLACNOM02 | placenta, neonatal F, NORM, WM | 1 | 0.0056 |
| LIVSFEM02 | liver/spleen, fetal M, NORM, WM | 2 | 0.0053 |

FIGURE 3C